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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/469,637ADATE: 07/16/97
TIME: 13:11:58

INPUT SET: S19007.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
23 (1) General Information:
45 (i) APPLICANT: GREENE, JOHN M
6 FLEISCHMANN, ROBERT D

7 (ii) TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR

8 (iii) NUMBER OF SEQUENCES: 10

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
11 (B) STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
12 (C) CITY: WASHINGTON
13 (D) STATE: DC
14 (E) COUNTRY: US
15 (F) ZIP: 20005-3934

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk
18 (B) COMPUTER: IBM PC compatible
19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

21 (vi) CURRENT APPLICATION DATA:

22 (A) APPLICATION NUMBER: US 08/469,637
23 (B) FILING DATE: 06-JUN-1995
24 (C) CLASSIFICATION:

25 (viii) ATTORNEY/AGENT INFORMATION:

26 (A) NAME: STEFFE, ERIC K
27 (B) REGISTRATION NUMBER: 36,688
28 (C) REFERENCE/DOCKET NUMBER: 1488.0710001

29 (ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: (202) 371-2600
31 (B) TELEFAX: (202) 371 2540.32 (2) INFORMATION FOR SEQ ID NO:1:
3334 (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 1527 base pairs
36 (B) TYPE: nucleic acid
37 (C) STRANDEDNESS: double

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/469,637ADATE: 07/16/97
TIME: 13:12:01

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47 (D) TOPOLOGY: linear
 48
 49 (ii) MOLECULE TYPE: DNA (genomic)
 50
 51
 52 (ix) FEATURE:
 53 (A) NAME/KEY: CDS
 54 (B) LOCATION: 46..1248
 55
 56 (ix) FEATURE:
 57 (A) NAME/KEY: sig_peptide
 58 (B) LOCATION: 46..106
 59
 60 (ix) FEATURE:
 61 (A) NAME/KEY: mat_peptide
 62 (B) LOCATION: 109..1248
 63
 64
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 66

67 CGCCCAGCCG CCGCCTCCAA GCCCCTGAGG TTTCCGGGGA CCACAC	ATG AAC AAG	54
	Met Asn Lys	
	-21 -20	
71 TTG CTG TGC GCG CTC GTG TTT CTG GAC ATC TCC ATT AAG TGG ACC		102
72 Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr		
73 -15 -10 -5		
75 ACC CAG GAA ACG TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC		150
76 Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr		
77 1 5 10		
79 TCT CAT CAG CTG TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA		198
80 Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys		
81 15 20 25 30		
83 CAA CAC TGT ACA GCA AAG TGG AAG ACC GTG TGC GCC CCT CCT GAC		246
84 Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp		
85 35 40 45		
87 CAC TAC TAC ACA GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC		294
88 His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys		
89 50 55 60		
91 AGC CCC GTG TGC AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC		342
92 Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg		
93 65 70 75		
95 ACC CAC AAC CGC GTG TGC 6AA TGC AAG GAA GGG CGC TAC CTT GAG ATA		390
96 Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile		
97 80 85 90		
99 GAG TTC TGC TTG AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG		438

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100	Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val			
101	95	100	105	110
102				
103	CAA GCT GGA ACC CCA GAG CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT	486		
104	Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp			
105	115	120	125	
106				
107	GGG TTC TTC TCA AAT GAG ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC	534		
108	Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His			
109	130	135	140	
110				
111	ACA AAT TGC AGT GTC TTT GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA	582		
112	Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala			
113	145	150	155	
114				
115	ACA CAC GAC AAC ATA TGT TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT	630		
116	Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys			
117	160	165	170	
118				
119	GGA ATA GAT GTT ACC CTG TGT GAG GAG GCA TTC TTC AGG TTT GCT GTT	678		
120	Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val			
121	175	180	185	190
122				
123	CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT GTC TTG GTA GAC AAT TTG	726		
124	Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu			
125	195	200	205	
126				
127	CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA GAG AGG ATA AAA CGG CAA	774		
128	Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln			
129	210	215	220	
130				
131	CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG CTG AAG TTA TGG AAA CAT	822		
132	His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His			
133	225	230	235	
134				
135	CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG ATC ATC CAA GAT ATT GAC	870		
136	Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp			
137	240	245	250	
138				
139	CTC TGT GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT AAC CTC ACC	918		
140	Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr			
141	255	260	265	270
142				
143	TTC GAG CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA AAG AAA GTG	966		
144	Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val			
145	275	280	285	
146				
147	GGA GCA GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA CCC AGT GAC	1014		
148	Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp			
149	290	295	300	
150				
151	CAG ATC CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT GGC GAC CAA	1062		
152	Gln Ile Leu Lys Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln			

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153	305	310	315	
154				
155	GAC ACC TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA AAG ACG TAC			1110
156	Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr			
157	320	325	330	
158				
159	CAC TTT CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC ATC AGG TTC			1158
160	His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe			
161	335	340	345	350
162				
163	CTT CAC AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA TTT TTA GAA			1206
164	Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu			
165	355	360	365	
166				
167	ATG ATA GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA			1248
168	Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu			
169	370	375	380	
170				
171	TAAC TGGAAA TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGAGTAA			1308
172				
173	ACTGTTCTC AGGCACATTGA GGCTTTCAGT GATATCTTC TCATTACCAG TGACTAATTT			1368
174				
175	TGCCACAGGG TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT CCTCCAATAA			1428
176				
177	ACCCCAAATG GTTAATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT ATATTTCCC			1488
178				
179	TTATTACTGC TTGCAGTAAT TCAACTGGAA AAAAAAAA			1527
180				
181				
182	(2) INFORMATION FOR SEQ ID NO:2:			
183				
184	(i) SEQUENCE CHARACTERISTICS:			
185	(A) LENGTH: 401 amino acids			
186	(B) TYPE: amino acid			
187	(D) TOPOLOGY: linear			
188				
189	(ii) MOLECULE TYPE: protein			
190				
191	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:			
192				
193	Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile			
194	-21 -20	-15	-10	
195				
196	Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp			
197	-5	1	5	10
198				
199	Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr			
200	15	20	25	
201				
202	Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro			
203	30	35	40	
204				
205	Cys Pro Asp His Tyr Tyr Asp Ser Trp His Thr Ser Asp Glu Cys			

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206 45 50 55
207
208 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
209 60 65 70 75
210
211 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
212 80 85 90
213
214 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
215 95 100 105
216
217 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
218 110 115 120
219
220 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
221 125 130 135
222
223 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
224 140 145 150 155
225
226 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
227 160 165 170
228
229 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
230 175 180 185
231
232 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
233 190 195 200
234
235 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
236 205 210 215
237
238 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
239 220 225 230 235
240
241 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
242 240 245 250
243
244 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
245 255 260 265
246
247 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
248 270 275 280
249
250 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
251 285 290 295
252
253 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
254 300 305 310 315
255
256 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
257 320 325 330
258

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/08/469,637A**

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Original Text